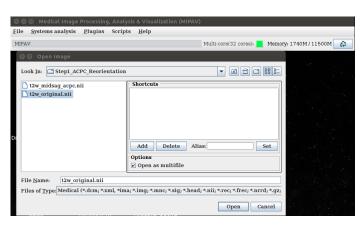
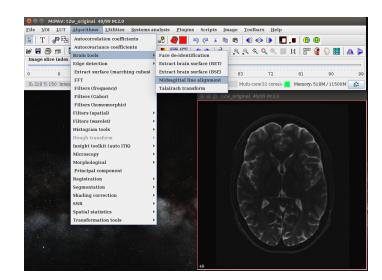
## STEP 1. ACPC reorientation of a structural Image

a) Open MIPAV. Open image from disk (under file menu). Open your original structural image.

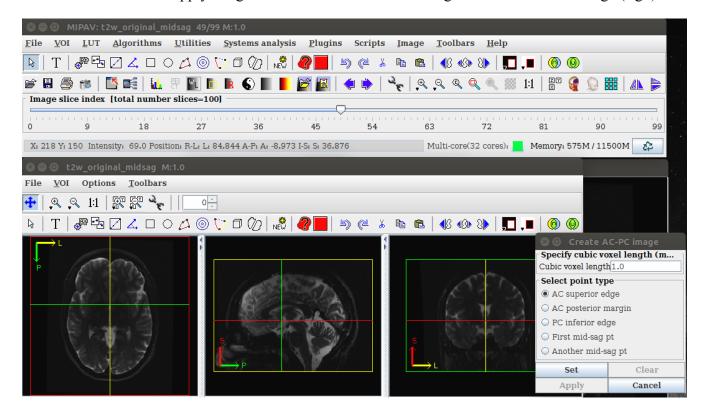


b) Perform midsagittal alignment (fig 2).



- \*To further understand about midsagittal alignment please visit: <a href="http://mipav.cit.nih.gov/pubwiki/index.php/Midsagittal\_line\_alignment">http://mipav.cit.nih.gov/pubwiki/index.php/Midsagittal\_line\_alignment</a>
- c) Select the generated image, perform Talairach transform (Algorithms-> Brain tools  $\rightarrow$  Talairach transform) and perform ACPC transform.

d) Select your Anterior Commissure, click "Set" twice. Select your Posterior Commissure, click "Set". Select a point in the cortical region, on the sagittal slice and "Set". Select another point on the sagittal slice and "Set". Then "Apply" to generate the final reoriented image and save the new image (fig3).



\* AC-PC alignment procedure and selection of points is detailed in the following manual: http://mipav.cit.nih.gov/documentation/presentations/talairach.pdf

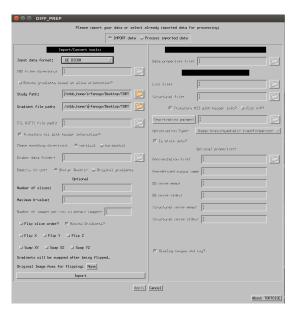
## STEP 2. DATA IMPORT in DIFFPREP

a) Load DIFFPREP gui as follows:

In a terminal (fig 4) go to the location where you have installed TORTOISE software. From here you can load DIFFPREP gui using the following path:

.../TORTOISE\_V2.1.0/DIFF\_PREP/diffprep\_main/prepvm

b) Make sure that the Import data radio button is checked on. Select the input data format from the drop down menu: For this example pick 'GE Dicom'



c) Load the study path:

...../TORTOISE tutorial 2014/Step2 Data Import/dti 35vol AP scan1/

d) Load the gradient file path:

...../TORTOISE tutorial 2014/Step2 Data Import/GE gradients.txt

e) Hit import

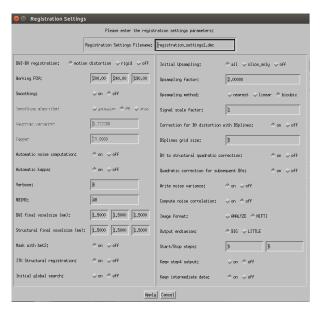
## STEP 3: DIFFPREP\_DMC

- a) Once the data is imported, in the same DIFFPREP gui the 'Process imported data' radio button will automatically get checked.
- b) List file: Here you will see the 'list file path' automatically selected.

(Note: When you import the data, a proc directory has been created outside the raw data folder. This proc directory contains: list file, path file and bmatrix file).

- c) Structural file: You will select the ACPC-aligned structural file.
- d) Registration params: select the default registration parameter file 'registration settings1.dmc'.

Note:Registration parameter settings can be edited to suit your output needs. You may edit the file by clicking on the button that says 'registration params'. You will see a Gui where you can edit the fields to tailor the registration output to your desired output resolution.



e) Optimization Type: select 'human brain/quadratic transformations'

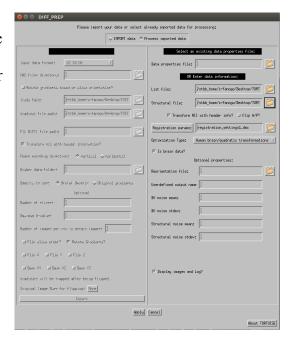
( note: there are three other transformations options under the drop down menu)

f) Hit Apply and the processing will begin.

The outputs will be as follows: up files: upsampled data

rpd files: transformation files

DMC files: distortion, motion corrected files

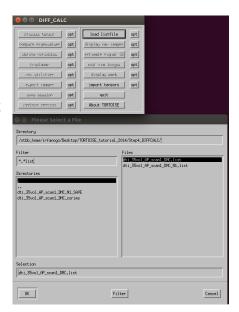


## STEP 4: DIFFCALC

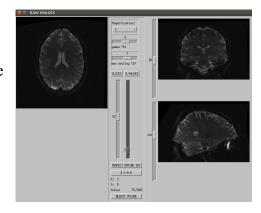
a) Load diffprep gui as follows:

In a terminal go to the location where you have installed TORTOISE software. From here you can load DIFFCALC gui using the following path: .../TORTOISE\_V2.1.0/DIFF\_CALC/diffcalc\_main/calcvm

b) In the GUI, please click on 'load images' button. Select the location that points to the \_proc directory. Pick the \_DMC.list file.

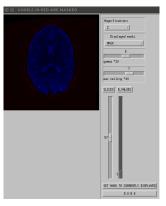


c) Click on the display raw images button to visually inspect the processed data, (fig 8).



Note: You may also click on "inspect entire set" button to view all the volumes and slices at the same time.

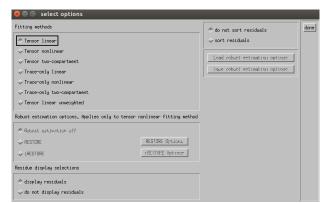
d) Hit done to go back to the DIFF\_CALC GUI



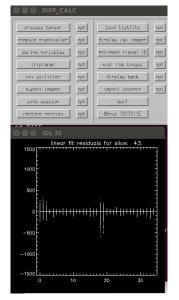
- e) Click on the estimate signal SD button. All the buttons will get inactive and you will see a residual window. This will go through all the slices and once complete, the buttons in the GUI will get activated.
- f) Click on mask raw images button.
- g) Display the mask and go through the slices to ensure that all the slices are masked correctly, (fig 9). Hit done to return to the main GUI.
- h) Process Tensor

Click on the 'opt' button next to the Process tensor button to open the tensor computation options GUI, (fig 10).

- I) Please select the appropriate tensor computation option by checking the radio button next to it. Hit done to return to the main GUI.
- j) Hit process tensor in the main GUI.



k) The process tensor when selected will open up another window showing the fitting residuals. When the tensor fitting is in progress, all the buttons in the main GUI will be inactivated, (fig 11). Upon completion, the buttons get activated.

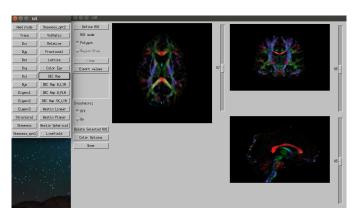


l) Click on roi utilities button to look at the tensor derived parameters (fig12). You can view the various parameters by clicking on the buttons. You can also draw roi's and save statistics.

To conclude session, click done. You will return to the main GUI.



m) You may also view the data in triplanar view. In the main GUI click on the triplanar button and you will see the window displayed.



DIFFPCALC processing details are available at the following location: <a href="https://science.nichd.nih.gov/confluence/display/nihpd/DIFF\_CALC+Main">https://science.nichd.nih.gov/confluence/display/nihpd/DIFF\_CALC+Main</a>